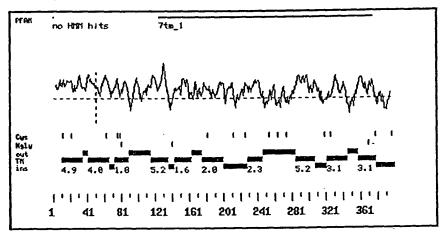
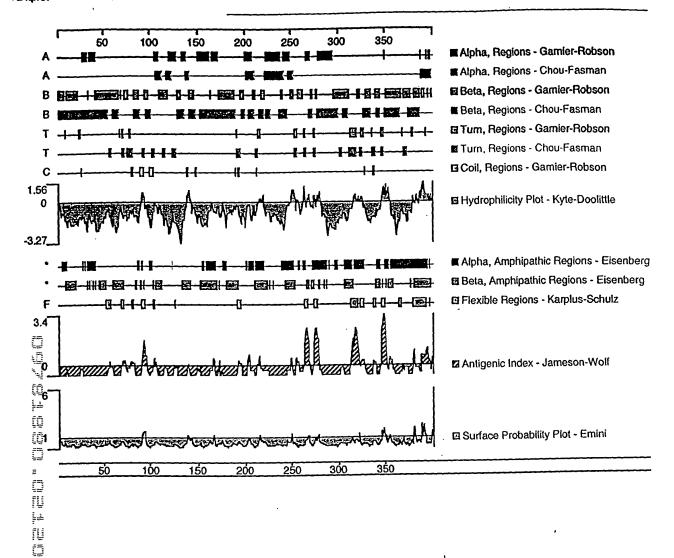
Analysis of 17724 (399 aa)

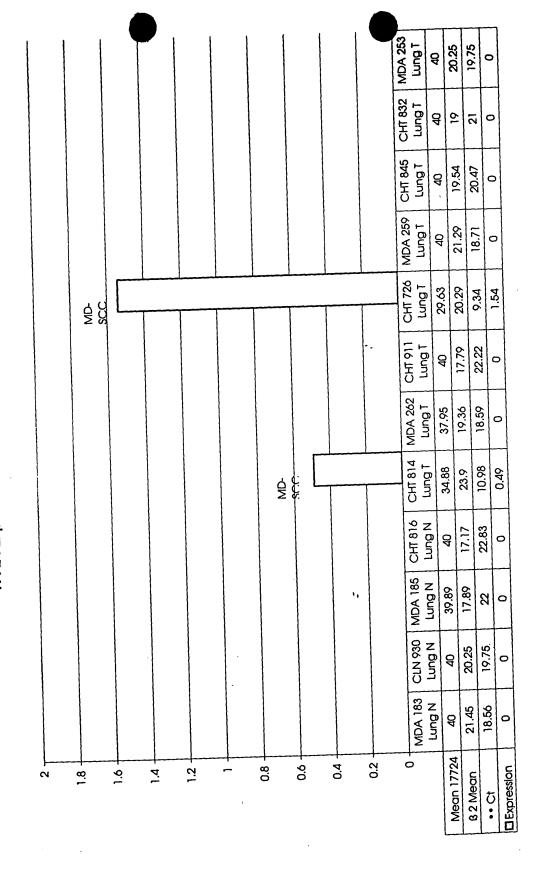


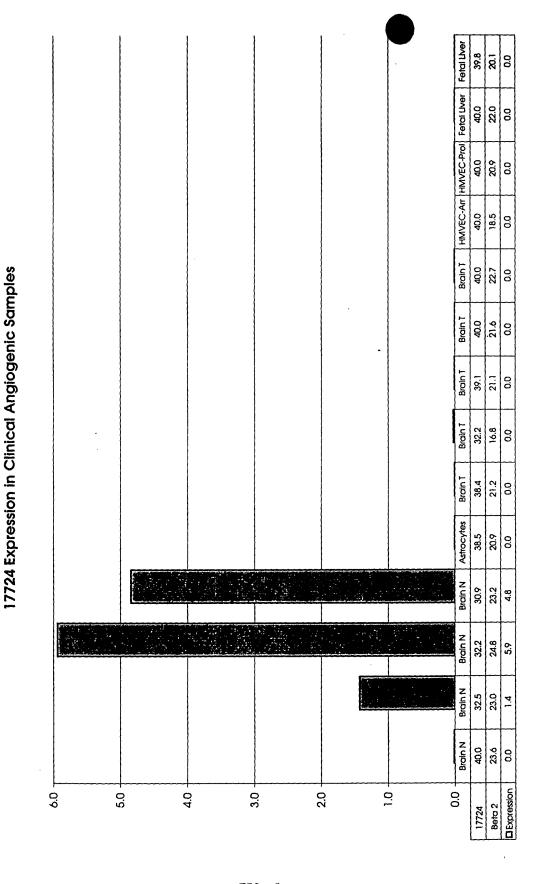


Query: 17724 Scores for sequence family classification (score includes all domains): Score E-value N Description 6.1e-29 1 7 transmembrane receptor (rhodopsin family) Parsed for domains: Model Domain seq-f seq-t hmm-f hmm-t score E-value 125 374 .. 1 259 [] 94.1 6.1e-29 1/1 7tm_1 Alignments of top-scoring domains: 7tm_1: domain 1 of 1, from 125 to 374: score 94.1, E = 6.1e-29 -->cNlLVilvilrtkklrtptnifilnLAVADLLfiltlppwalyylvg GN ++i+ ++ +l+tp+++f++N ++ +L++ t +p +l+ 1+ GNTIIIVMVIADTHLHTPMYFFLGNFSLLEILVTMTAVPRMLSDLLV 171 17724 125 gsedWpfGsalCklvtaldvvnmyaSillLtaISiDRYlAIvhPlryrrr ++++ +C ++ ++ + ++ S l Lt +++DR++AI+hPlry ++ 17724 172 -- PHKVITFTGCMVQFYFHFSLGSTSFLILTDMALDRFVAICHPLRYGTL 219 $rtsprrAkvvillv \verb|WvlalllslPpllfswvktveegngtlnvnvtvCli|$ ++ + ++ +++W++ +1+ +P ++8 ++ + +g+ +n+++C+ 220 MS-RAMCVQLAGAAWAAPFLAMVPT-VLSRAHLDYCHGGV--INHFFCDN 265 17724 dfpeestasvstwlrsyvllstlygFllPilvilvcYtrIlrtlr.... + ++8+ 1+++ +1 1 + 1 +lv 1+ Y+ I+ t+ + ++ 266 EPLLQLSCSDTRLLEFWDFLMALTFVLSSFLVTLISYGYIVTTVLripsa 315 ... kaaktll vvvvv FvlCWlPy fivl1ldtlc. 1 siims stCelervlptallvtlwLayvNsclNPiIY<-* + v+1+ +++ + 1NP+I 17724 354 VRKVVALVTSVLTPFLNPFIL

10 10.31 10.31 10.31 10.31 10.31 10.31 10.31 10.31 10.31 10.31 10.31 10.31 10.31 10.31 10.31 10.31 10.31 10.31

17724 Expression in Clinical Lung Samples





17724 CV II

0.024

0.114

0.136

0.712

0.990

FIG. 6

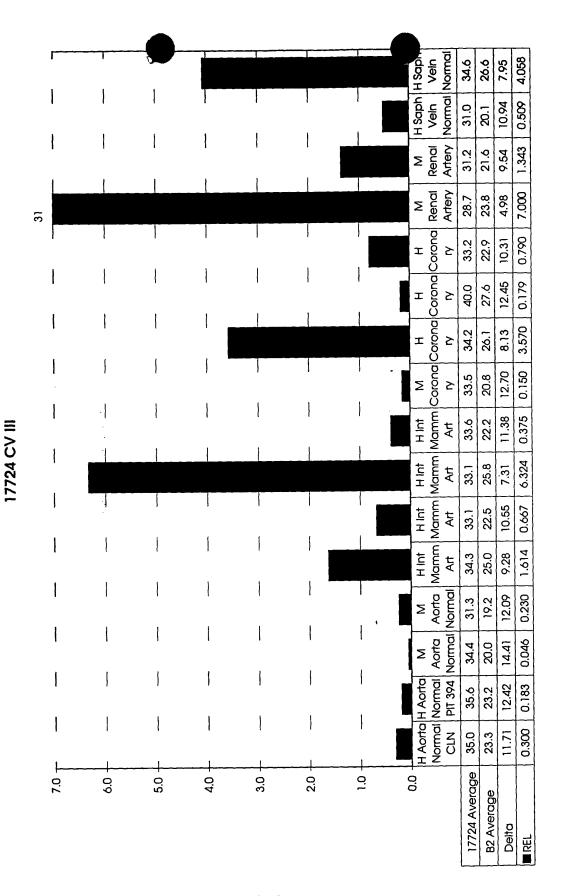
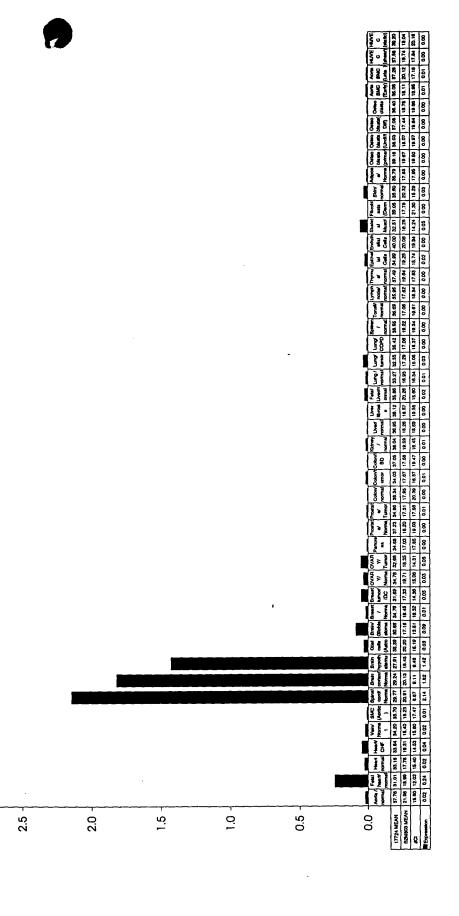


FIG. 7

Phase 1.2.1 expression of 17724

3.0



Analysis of 31945 (663 aa)

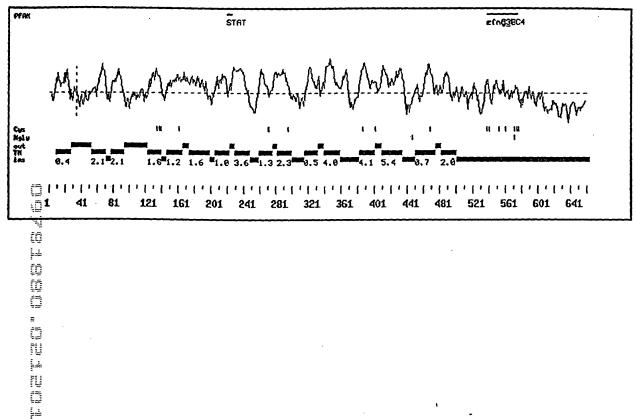
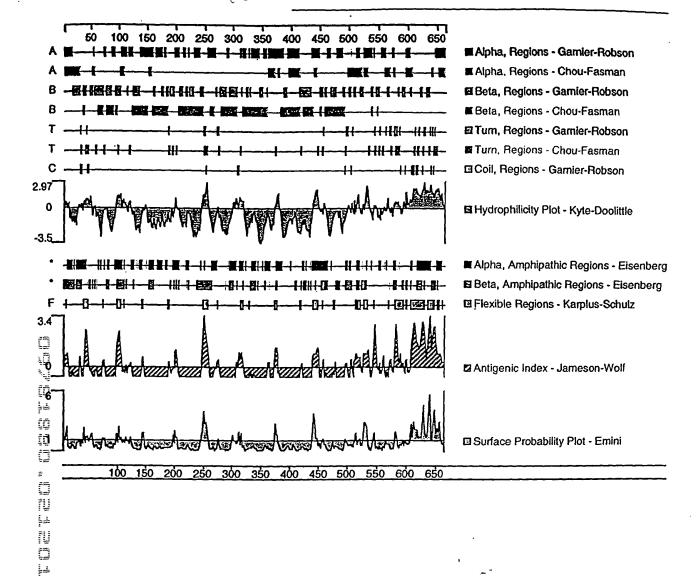
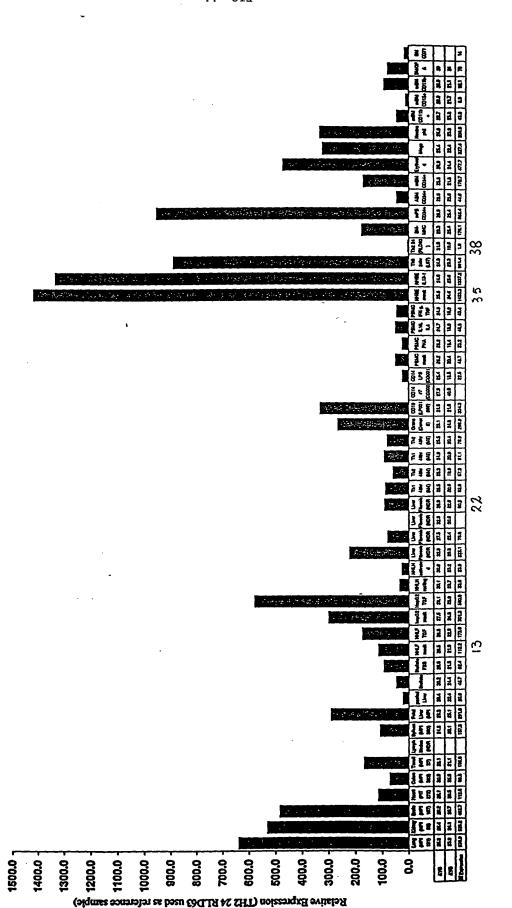


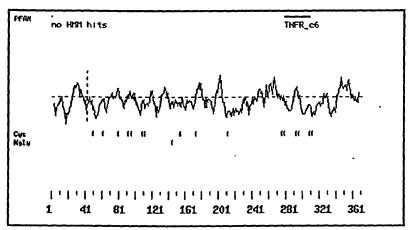
FIG. 9

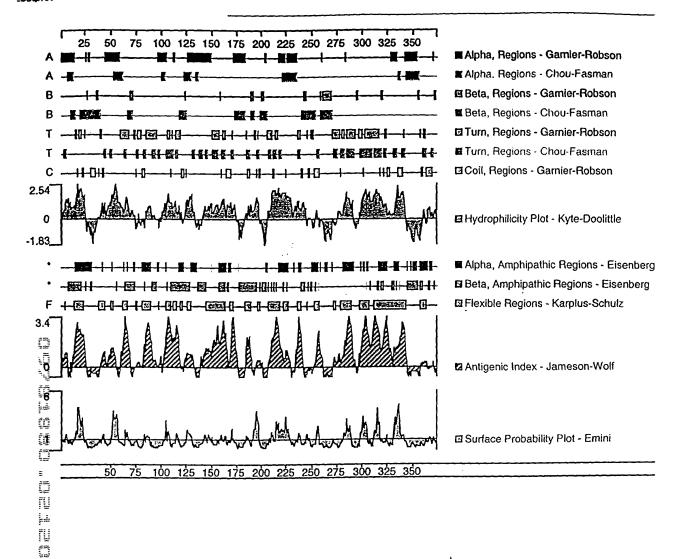


GPCR 31945 Expression



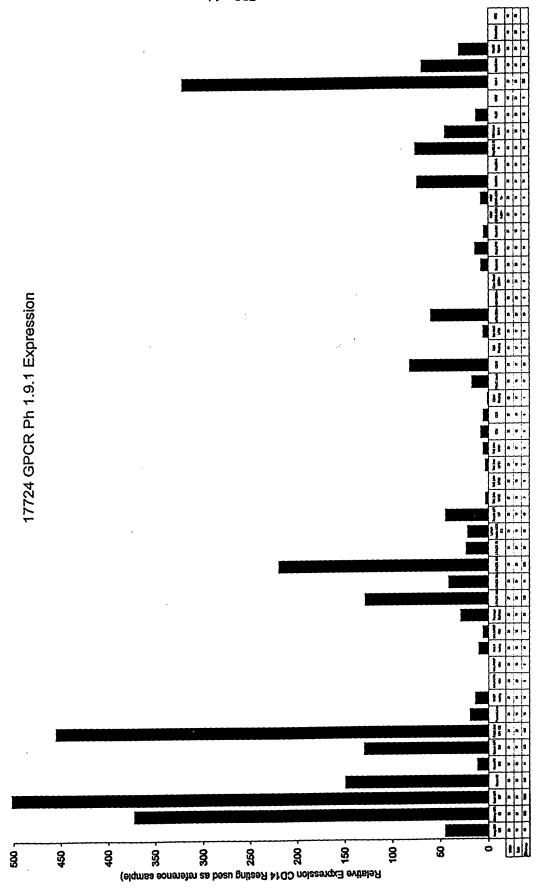
Analysis of 50288 (372 aa)



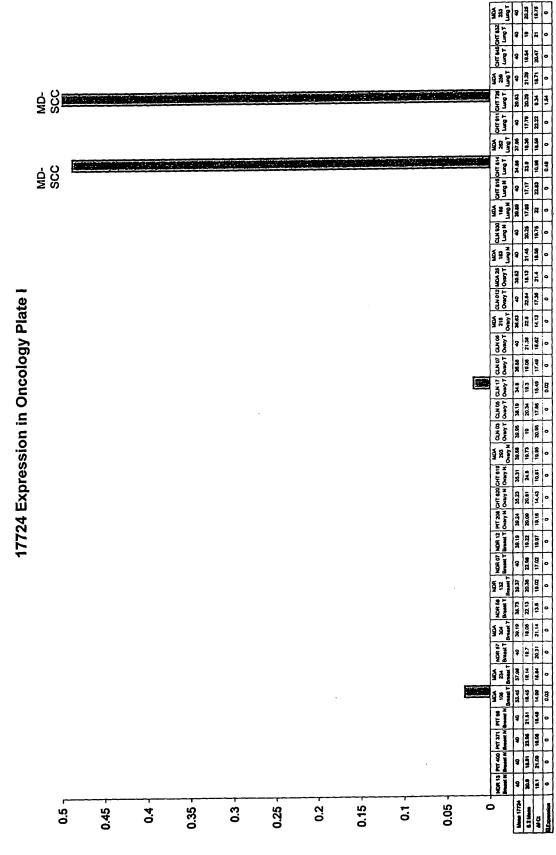


SCANNED, # 6

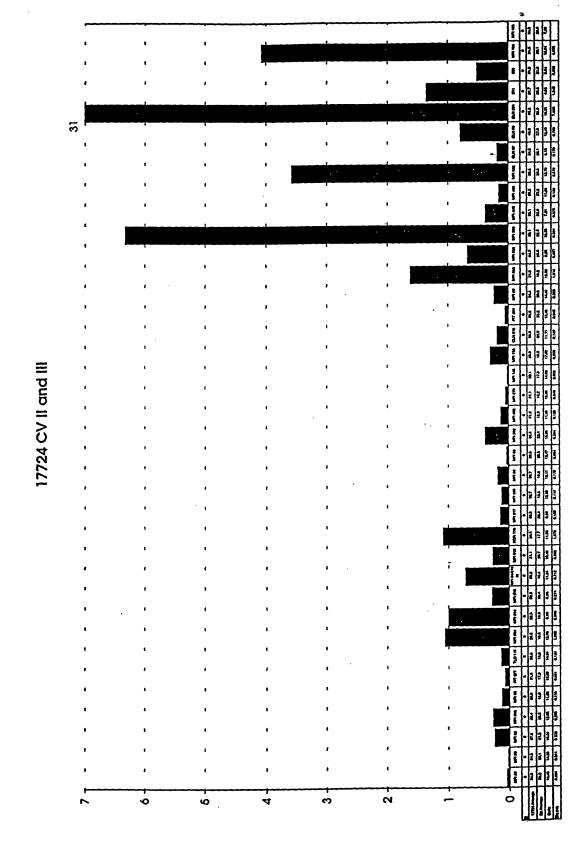
Taqman Chart+Table



EIG. 15



SCANNED, #



SCANNED, # 6

CI ne cbhTb018f11jt

